

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>09/637,302</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input checked="" type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> 7. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies primarily to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: <b>(2) INFORMATION FOR SEQ ID NO:X:</b> <b>(i) SEQUENCE CHARACTERISTICS:</b> (Do not insert any headings under "SEQUENCE CHARACTERISTICS") <b>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:</b> This sequence is intentionally skipped	
	Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response.	
12 <input checked="" type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> #7 are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/637,302

DATE: 08/23/2000  
TIME: 09:32:54

Input Set : A:\TSR7102.txt  
Output Set: N:\CRF3\08232000\I637302.raw

3 <110> APPLICANT: HOOD, John  
4 ELICEIRI, Brian  
5 CHERESH, David  
7 <120> TITLE OF INVENTION: Methods and Compositions Useful for Modulation of  
8 Angiogenesis Using Tyrosine Kinase Raf and Ras  
10 <130> FILE REFERENCE: TSRI 710.2  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/637,302  
C--> 13 <141> CURRENT FILING DATE: 2000-08-11  
15 <150> PRIOR APPLICATION NUMBER: US 60/148,924  
16 <151> PRIOR FILING DATE: 1999-08-13  
18 <150> PRIOR APPLICATION NUMBER: US 60/215,951  
19 <151> PRIOR FILING DATE: 2000-07-05  
21 <160> NUMBER OF SEQ ID NOS: 7  
23 <170> SOFTWARE: PatentIn Ver. 2.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 2977  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Homo sapiens  
30 <220> FEATURE:  
31 <221> NAME/KEY: CDS /  
32 <222> LOCATION: (130)..(2073)  
34 <400> SEQUENCE: 1  
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37 tgccggcaa cgacaggacg tggggcggc ctggctccct caggttaag aattgttaa 120  
39 gtcgcata atg gag cac ata cag gga gct tgg aag acg atc acg aat ggt 171  
40 Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly  
41 1 5 10  
43 ttt gga ttc aaa gat gcc gtg ttt gat ggc tcc acg tgc atc tct cct 219  
44 Phe Gly Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro  
45 15 20 25 30  
47 aca ata gtt cag cag ttt ggc tat cag cgc cgg gca tca gat gat ggc 267  
48 Thr Ile Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly  
49 35 40 45  
51 aaa ctc aca gat cct tct aag aca aac act atc cgt gtt ttc ttg 315  
52 Lys Leu Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu  
53 50 55 60  
55 ccg aac aag caa aca gca gtc aat gtg cga aat gga atg acg ttg 363  
56 Pro Asn Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu  
57 65 70 75  
59 cat gac tgc ctt atg aaa gca ctc aag gtg agg ggc ctg caa cca gag 411  
60 His Asp Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu  
61 80 85 90  
63 tgc tgt gca gtg ttc aga ctt ctc cac gaa cac aaa ggt aaa aaa gca 459  
64 Cys Cys Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala  
65 95 100 105 110  
67 cgc tta gat tgg aat act gat gct gcg tct ttg att gga gaa gaa ctt 507  
68 Arg Leu Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu

Does Not Comply  
Corrected Diskette Needed

See

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RAW SEQUENCE LISTING DATE: 08/23/2000  
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Input Set : A:\TSR7102.txt  
 Output Set: N:\CRF3\08232000\I637302.raw

69	115	120	125	
71	caa gta gat ttc ctg gat cat gtt ccc ctc aca aca cac aac ttt gct			555
72	Gln Val Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala			
73	130	135	140	
75	cgg aag acg ttc ctg aag ctt gcc ttc tgt gac atc tgt cag aaa ttc			603
76	Arg Lys Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe			
77	145	150	155	
79	ctg ctc aat gga ttt cga tgt cag act tgt ggc tac aaa ttt cat gag			651
80	Leu Leu Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu			
81	160	165	170	
83	cac tgt agc acc aaa gta cct act atg tgt gtc gac tgg aat aac atc			699
84	His Cys Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile			
85	175	180	185	190
87	aga caa ctc tta ttg ttt cca aat tcc act att ggt gat agt gga gtc			747
88	Arg Gln Leu Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val			
89	195	200	205	
91	cca gca cta cct tct ttg act atg cgt cgt atg cga gag tct gtt tcc			795
92	Pro Ala Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser			
93	210	215	220	
95	agg atg cct gtt agt tct cag cac aga tat tct aca cct cac gcc ttc			843
96	Arg Met Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe			
97	225	230	235	
99	acc ttt aac acc tcc agt ccc tca tct gaa ggt tcc ctc tcc cag agg			891
100	Thr Phe Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg			
101	240	245	250	
103	cag agg tcg aca tcc aca cct aat gtc cac atg gtc agc acc acg ctg			939
104	Gln Arg Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu			
105	255	260	265	270
107	cct gtg gac agc agg atg att gag gat gca att cga agt cac agc gaa			987
108	Pro Val Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu			
109	275	280	285	
111	tca gcc tca cct tca gcc ctg tcc agt agc ccc aac aat ctg agc cca			1035
112	Ser Ala Ser Pro Ser Ala Leu Ser Ser Pro Asn Asn Leu Ser Pro			
113	290	295	300	
115	aca ggc tgg tca cag ccg aaa acc ccc gtg cca gca caa aga gag cgg			1083
116	Thr Gly Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg			
117	305	310	315	
119	gca cca gta tct ggg acc cag gag aaa aac aaa att agg cct cgt gga			1131
120	Ala Pro Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly			
121	320	325	330	
123	cag aga gat tca agc tat tat tgg gaa ata gaa gcc agt gaa gtg atg			1179
124	Gln Arg Asp Ser Ser Tyr Tyr Trp Glu Ile Glu Ala Ser Glu Val Met			
125	335	340	345	350
127	ctg tcc act cgg att ggg tca ggc tct ttt gga act gtt tat aag ggt			1227
128	Leu Ser Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly			
129	355	360	365	
131	aaa tgg cac gga gat gtt gca gta aag atc cta aag gtt gtc gac cca			1275
132	Lys Trp His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro			
133	370	375	380	

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PATENT APPLICATION: US/09/637,302

DATE: 08/23/2000  
TIME: 09:32:54

Input Set : A:\TSR7102.txt  
Output Set: N:\CRF3\08232000\1637302.raw

135	acc cca gag caa ttc cag gcc ttc agg aat gag gtg gct gtt ctg cgc	1323
136	Thr Pro Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg	
137	385 390 395	
139	aaa aca cgg cat gtg aac att ctg ctt ttc atg ggg tac atg aca aag	1371
140	Lys Thr Arg His Val Asn Ile Leu Leu Phe Met Gly Tyr Met Thr Lys	
141	400 405 410	
143	gac aac ctg gca att gtg acc cag tgg tgc gag ggc agc agc ctc tac	1419
144	Asp Asn Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr	
145	415 420 425 430	
147	aaa cac ctg cat gtc cag gag acc aag ttt cag atg ttc cag cta att	1467
148	Lys His Leu His Val Gln Glu Thr Lys Gln Met Phe Gln Leu Ile	
149	435 440 445	
151	gac att gcc cgg cag acg gct cag gga atg gac tat ttg cat gca aag	1515
152	Asp Ile Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys	
153	450 455 460	
155	aac atc atc cat aga gac atg aaa tcc aac aat ata ttt ctc cat gaa	1563
156	Asn Ile Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu	
157	465 470 475	
159	ggc tta aca gtg aaa att gga gat ttt ggt ttg gca aca gta aag tca	1611
160	Gly Leu Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser	
161	480 485 490	
163	cgc tgg agt ggt tct cag cag gtt gaa caa cct act ggc tct gtc ctc	1659
164	Arg Trp Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu	
165	495 500 505 510	
167	tgg atg gcc cca gag gtg atc cga atg cag gat aac aac cca ttc agt	1707
168	Trp Met Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser	
169	515 520 525	
171	tcc cag tcc gat gtc tac tcc tat ggc atc gta ttg tat gaa ctg atg	1755
172	Phe Gln Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met	
173	530 535 540	
175	acg ggg gag ctt cct tat tct cac atc aac aac cga gat cag atc atc	1803
176	Thr Gly Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile	
177	545 550 555	
179	tcc atg gtg ggc cga gga tat gcc tcc cca gat ctt agt aag cta tat	1851
180	Phe Met Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr	
181	560 565 570	
183	aag aac tgc ccc aaa gca atg aag agg ctg gta gct gac tgt gtg aag	1899
184	Lys Asn Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys	
185	575 580 585 590	
187	aaa gta aag gaa gag agg cct ctt ttt ccc cag atc ctg tct tcc att	1947
188	Lys Val Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile	
189	595 600 605	
191	gag ctg ctc caa cac tac tct cta ccg aag atc aac cgg agc gct tcc gag	1995
192	Glu Leu Leu Gln His Ser Leu Pro Lys Ile Asn Arg Ser Ala Ser Glu	
193	610 615 620	
195	cca tcc ttg cat cgg gca gcc cac act gag gat atc aat gct tgc acg	2043
196	Pro Ser Leu His Arg Ala Ala His Thr Glu Asp Ile Asn Ala Cys Thr	
197	625 630 635	
199	ctg acc acg tcc ccg agg ctg cct gtc ttc tagttgactt tgcacctgtc	2093

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Input Set : A:\TSR7102.txt  
 Output Set: N:\CRF3\08232000\I637302.raw

200 Leu Thr Thr Ser Pro Arg Leu Pro Val Phe  
 201 640 645  
 203 ttcaggtgc caggggagga ggaaggcca gcaggcacca ctttctgct cccttcctcc 2153  
 205 agaggcagaa cacatgttt cagagaagct ctgctaaagga ctttctagac tgctcacagg 2213  
 207 gccttaactt catgttgcct tctttctat cccttgggc cttggagaa ggaaggccat 2273  
 209 tgcagtgctg gtgtgtcctg ctcocctcccc acatccccca tgctcaaggc ccagcttct 2333  
 211 gtagatgcgc aagtggatgt tgatggatgt aaaaaaagca ggggccccagc cccagctgtt 2393  
 213 ggctacatga tgatttagag gaagtaaggt agcaggcagt ccagccctga tggagaca 2453  
 215 catgggattt tggaaatcag cttctggagg aatgcacatgtc acaggcgaa ctttcttcag 2513  
 217 agagtggtgc agcggccagac atttgcaca taaggcacca aacagccca gactgcccag 2573  
 219 actctggccg cccgaaggag cctgttgg tactatggaa ctttcttag gggacacgtc 2633  
 221 ctcccttcac agtcttaag gtgtccagtg cattggatgt gttttccagg caaggcactc 2693  
 223 ggccaatccg catctcagcc ctctcaggag cagtcttcca tcatgctgaa ttttgttcttc 2753  
 225 caggagctgc cccatgggg cggccgcag ggcacgcctg tttctctaac aaacaaacaa 2813  
 227 acaaacaccc ttgtttctt agtcacatca tggtatatac aggaagccag gaatacaggt 2873  
 229 tttcttgatg atttgggtt taatttgtt ttatggcactgacatc 2933  
 231 gatggccct caattatgtt atttataaa aataaattaa attt 2977  
 234 <210> SEQ ID NO: 2  
 235 <211> LENGTH: 648  
 236 <212> TYPE: PRT  
 237 <213> ORGANISM: Homo sapiens  
 239 <400> SEQUENCE: 2  
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 241 1 5 10 15  
 243 Phe Lys Asp Ala Val Phe Asp Gly Ser Ser Cys Ile Ser Pro Thr Ile  
 244 20 25 30  
 246 Val Gln Gln Phe Gly Tyr Gln Arg Arg Ala Ser Asp Asp Gly Lys Leu  
 247 35 40 45  
 249 Thr Asp Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn  
 250 50 55 60  
 252 Lys Gln Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp  
 253 65 70 75 80  
 255 Cys Leu Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys  
 256 85 90 95  
 258 Ala Val Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu  
 259 100 105 110  
 261 Asp Trp Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val  
 262 115 120 125  
 264 Asp Phe Leu Asp His Val Pro Leu Thr Thr His Asn Phe Ala Arg Lys  
 265 130 135 140  
 267 Thr Phe Leu Lys Leu Ala Phe Cys Asp Ile Cys Gln Lys Phe Leu Leu  
 268 145 150 155 160  
 270 Asn Gly Phe Arg Cys Gln Thr Cys Gly Tyr Lys Phe His Glu His Cys  
 271 165 170 175  
 273 Ser Thr Lys Val Pro Thr Met Cys Val Asp Trp Ser Asn Ile Arg Gln  
 274 180 185 190  
 276 Leu Leu Leu Phe Pro Asn Ser Thr Ile Gly Asp Ser Gly Val Pro Ala  
 277 195 200 205  
 279 Leu Pro Ser Leu Thr Met Arg Arg Met Arg Glu Ser Val Ser Arg Met

RAW SEQUENCE LISTING DATE: 08/23/2000  
 PATENT APPLICATION: US/09/637,302 TIME: 09:32:54

Input Set : A:\TSR7102.txt  
 Output Set: N:\CRE3\08232000\I637302.raw

280	210	215	220
282	Pro Val Ser Ser Gln His Arg Tyr Ser Thr Pro His Ala Phe Thr Phe		
283	225	230	235
285	Asn Thr Ser Ser Pro Ser Ser Glu Gly Ser Leu Ser Gln Arg Gln Arg		240
286	245	250	255
288	Ser Thr Ser Thr Pro Asn Val His Met Val Ser Thr Thr Leu Pro Val		
289	260	265	270
291	Asp Ser Arg Met Ile Glu Asp Ala Ile Arg Ser His Ser Glu Ser Ala		
292	275	280	285
294	Ser Pro Ser Ala Leu Ser Ser Pro Asn Asn Leu Ser Pro Thr Gly		
295	290	295	300
297	Trp Ser Gln Pro Lys Thr Pro Val Pro Ala Gln Arg Glu Arg Ala Pro		
298	305	310	315
300	Val Ser Gly Thr Gln Glu Lys Asn Lys Ile Arg Pro Arg Gly Gln Arg		320
301	325	330	335
303	Asp Ser Ser Tyr Trp Glu Ile Glu Ala Ser Glu Val Met Leu Ser		
304	340	345	350
306	Thr Arg Ile Gly Ser Gly Ser Phe Gly Thr Val Tyr Lys Gly Lys Trp		
307	355	360	365
309	His Gly Asp Val Ala Val Lys Ile Leu Lys Val Val Asp Pro Thr Pro		
310	370	375	380
312	Glu Gln Phe Gln Ala Phe Arg Asn Glu Val Ala Val Leu Arg Lys Thr		
313	385	390	395
315	Arg His Val Asn Ile Leu Phe Met Gly Tyr Met Thr Lys Asp Asn		400
316	405	410	415
318	Leu Ala Ile Val Thr Gln Trp Cys Glu Gly Ser Ser Leu Tyr Lys His		
319	420	425	430
321	Leu His Val Gln Glu Thr Lys Phe Gln Met Phe Gln Leu Ile Asp Ile		
322	435	440	445
324	Ala Arg Gln Thr Ala Gln Gly Met Asp Tyr Leu His Ala Lys Asn Ile		
325	450	455	460
327	Ile His Arg Asp Met Lys Ser Asn Asn Ile Phe Leu His Glu Gly Leu		
328	465	470	475
330	Thr Val Lys Ile Gly Asp Phe Gly Leu Ala Thr Val Lys Ser Arg Trp		480
331	485	490	495
333	Ser Gly Ser Gln Gln Val Glu Gln Pro Thr Gly Ser Val Leu Trp Met		
334	500	505	510
336	Ala Pro Glu Val Ile Arg Met Gln Asp Asn Asn Pro Phe Ser Phe Gln		
337	515	520	525
339	Ser Asp Val Tyr Ser Tyr Gly Ile Val Leu Tyr Glu Leu Met Thr Gly		
340	530	535	540
342	Glu Leu Pro Tyr Ser His Ile Asn Asn Arg Asp Gln Ile Ile Phe Met		
343	545	550	555
345	Val Gly Arg Gly Tyr Ala Ser Pro Asp Leu Ser Lys Leu Tyr Lys Asn		560
346	565	570	575
348	Cys Pro Lys Ala Met Lys Arg Leu Val Ala Asp Cys Val Lys Lys Val		
349	580	585	590
351	Lys Glu Glu Arg Pro Leu Phe Pro Gln Ile Leu Ser Ser Ile Glu Leu		
352	595	600	605

09/637, 30

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Seg # 7

<210> 7  
<211> 668  
<212> PRT  
<213> Artificial Sequence

<400> 7

Met Glu His Ile Gln Gly Ala Trp Lys Thr Ile Ser Asn Gly Phe Gly  
1 5 10 15

missing mandatory <220> and <223> features to  
explain artificial sequence. See #12 on  
Error Summary Sheet. \*Also see #7 on  
Error Summary Sheet

VERIFICATION SUMMARY DATE: 08/23/2000  
PATENT APPLICATION: US/09/637,302 TIME: 09:32:55

Input Set : A:\TSR7102.txt  
Output Set: N:\CRF3\08232000\I637302.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:892 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:892 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: